LUNA ZEA-REDONDO, Ph.D.

Computational Biologist | Multi-Omics & Translational Research

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SUMMARY

Computational Biologist with **10+ years of experience** applying quantitative and statistical approaches to complex biological systems, spanning **cancer genomics** to neuroepigenetics. **PhD in Systems Biology** with strong expertise in **multi-omics** and time-course data analysis. Experienced in building **reproducible analytical workflows** and collaborating across **interdisciplinary** research teams. Seeking to apply computational rigor to translational and clinically relevant research challenges.

SKILLS

- **Computational Biology & Multi-Omics**: Bulk and single-cell RNA-seq, ATAC-seq, and ChIP-seq data processing, mapping, and QC; epigenomic and transcriptomic analysis; multi-omics integration; time-course modeling, applied ML for high-dimensional omics data.
- **Programming & Analytical Ecosystem**: Python (NumPy, Pandas, Scikit-learn, Scanpy), R (Bioconductor, DESeq2, edgeR, Seurat), Shell, SQL; Git, Docker; cloud-based data analysis (GCP, BigQuery).
- **Project Management & Communication**: Cross-functional teamwork, project planning, mentoring, scientific writing, peer review for international journals, oral presentations at conferences.

PROFESSIONAL EXPERIENCE

Senior Research Scientist | Computational Biology **Oct 2025 – present**
Berlin Institute for Medical Systems Biology (MDC-BIMSB) *Berlin, Germany*

- **Lead** the end-to-end delivery of a **first-author multi-omics study** through manuscript submission, integrating project design, experimental execution, large-scale data processing, computational analysis, and scientific interpretation in alignment with senior stakeholders.
- **Initiated** and coordinated **two collaborative research projects** derived from my doctoral work, coordinating delivery across **four international cross-functional teams**.
- **Mentor** junior researchers in experimental design and computational analysis, and serve as a **peer reviewer** for international scientific journals.

Ph.D. Researcher | Computational Biology **Jan 2019 – Oct 2025**
Berlin Institute for Medical Systems Biology (MDC-BIMSB) *Berlin, Germany*

- **Designed** and executed a **large-scale single-cell multi-omics** study (18 samples, >150,000 cells, 6 time points) covering preprocessing and QC, differential analyses, and time-course modeling to uncover regulatory mechanisms of cellular memory in **addiction-relevant neuronal systems**.
- **Generated and analyzed >10 large-scale genomic** (single-cell RNA and ATAC, bulk ATAC and ChIP-seq) datasets, contributing to five scientific publications.
- **Co-led** a collaborative multi-omics project culminating in a **co-first-author *Nature* (2021) publication** (>200 citations), integrating scRNA-seq, scATAC-seq, and 3D genome topology across brain cell types.

- **Developed** robust, reusable **analytical workflows** adopted across the group, improving reproducibility and standardizing analysis practices.
- **Mentored** junior researchers in experimental design and computational analysis and contributed as **a peer reviewer** for 5+ international scientific journals.

Junior Scientist | Cancer Genomics & Computational Biology **Feb 2017 – Aug 2018**
New York University Medical School (NYUMS). *New York, US*

- **Investigated** the functional impact of MED12 mutations in **chronic lymphocytic leukemia**, generating and analyzing **>20 ChIP-, RNA-, and ATAC-seq datasets** from primary patient blood samples and cell lines.
- **Analyzed** > **10 ChIP-seq and ATAC-seq datasets** for studies on inflammation and leukemic transformation contributing to **high-impact publications** (*Nature Immunology* and *Cell Stem Cell*).

Research Fellow | Molecular Biology & Functional Genomics **Oct 2015 – Sep 2016**
European Molecular Biology Laboratory (EMBL) *Rome, Italy*
Max-Planck-Institute for Molecular Genetics (MPIMG) *Berlin, Germany*

- Conducted **hands-on molecular biology** work bridging wet-lab and computational expertise across two leading European research institutes.

EDUCATION

PhD in Systems Biology • Humboldt University of Berlin • Berlin, Germany (*Summa cum laude*) • **2025**
MSc in Bioinformatics • Autonomous University of Barcelona • Barcelona, Spain • **2017**
BSc in Biochemistry and Molecular Biology • University of Córdoba • Córdoba, Spain • **2015**

SELECTED PUBLICATIONS

1. **Zea-Redondo, L.** (2021). *Cell-type specialization is encoded by specific chromatin topologies.* **Nature**, 599, 684–691. (*Shared first authorship*)
2. Muto, T. et al. (2022). *TRAF6 functions as a tumor suppressor in myeloid malignancies by directly targeting MYC oncogenic activity.* **Cell Stem Cell**, 29(2), 298–314.e9.
3. Guillamot, M. et al. (2019). *The E3 ubiquitin ligase SPOP controls resolution of systemic inflammation by triggering MYD88 degradation.* **Nature Immunology**, 20, 1196–1207.

📊 Full project details, publications, and additional materials at: **red-moonx.github.io**